

We claim:

1. A process for the production of polyunsaturated fatty acids in an organism, which comprises the following steps:
  - 5 a) introducing, into the organism, at least one nucleic acid sequence with the sequence shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18 or SEQ ID NO: 20, which codes for a polypeptide with lysophosphatidic acid acyltransferase activity;
    - 10 or
    - b) introducing, into the organism, at least one nucleic acid sequence with the sequence shown in SEQ ID NO: 22, SEQ ID NO: 24 or SEQ ID NO: 26, which codes for a polypeptide with glycerol-3-phosphate acyltransferase activity; or
    - 15 c) introducing, into the organism, at least one nucleic acid sequence with the sequence shown in SEQ ID NO: 28, SEQ ID NO: 30 or SEQ ID NO: 32 which codes for a polypeptide with diacylglycerol acyltransferase activity;
      - or
      - 20 d) introducing, into the organism, at least one nucleic acid sequence with the sequence shown in SEQ ID NO: 34 or SEQ ID NO: 36, which codes for a polypeptide with lecithin cholesterol acyltransferase activity; or
      - e) introducing, into the organism, at least one nucleic acid sequence which can be derived from the coding sequence in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34 or SEQ ID NO: 36 as the result of the degeneracy of the genetic code, or
      - 25 f) introducing, into the organism, at least one derivative of the nucleic acid sequence shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34 or SEQ ID NO: 36, which code for polypeptides with the amino acid sequence shown in SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35 or SEQ ID NO: 37 and which have at least 40%
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homology at the amino acid level with SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35 or SEQ ID NO: 37 and have an equivalent lysophosphatidic acid acyltransferase activity, glycerol-3-phosphate acyltransferase activity, diacylglycerol acyltransferase activity or lecithin cholesterol acyltransferase activity, and

g) culturing and harvesting the organism.

2. The process for the production of polyunsaturated fatty acids according to claim 1, wherein, additionally to the nucleic acid sequences mentioned under (a) to (f), further nucleic acid sequences which code for polypeptides of the fatty acid metabolism or lipid metabolism selected from the group consisting of acyl-CoA dehydrogenase(s), acyl-ACP[= acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyltransferase(s), acyl-CoA:lysophospholipid acyltransferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenase(s), lipoxygenase(s), triacylglycerol lipase(s), allene oxide synthase(s), hydroperoxide lyase(s) or fatty acid elongase(s) were introduced into the organism.
3. The process for the production of polyunsaturated fatty acids according to claim 1 or 2, wherein, additionally to the nucleic acid sequences mentioned under (a) to (f), further nucleic acid sequences which code for polypeptides selected from the group consisting of acyl-CoA:lysophospholipid acyltransferase,  $\Delta$ -4-desaturase,  $\Delta$ -5-desaturase,  $\Delta$ -6-desaturase,  $\Delta$ -8-desaturase,  $\Delta$ -9-desaturase,  $\Delta$ -12-desaturase,  $\Delta$ -5-elongase,  $\Delta$ -6-elongase or  $\Delta$ -9-elongase, were introduced into the organism.
4. The process for the production of polyunsaturated fatty acids according to any of claims 1 to 3, wherein the polyunsaturated fatty acids produced are  $C_{18-}$ ,  $C_{20-}$ ,  $C_{22-}$  or  $C_{24-}$ -fatty acids.
5. The process for the production of polyunsaturated fatty acids according to any of claims 1 to 4, wherein the polyunsaturated fatty acids are isolated from the organism in the form of an oil, a lipid or a free fatty acid.
6. The process for the production of polyunsaturated fatty acids according to any of claims 1 to 5, wherein the polyunsaturated fatty acids produced in the process are  $C_{18-}$ ,  $C_{20-}$ ,  $C_{22-}$  or  $C_{24-}$ -fatty acids with at least two double bonds in the molecule.
7. The process for the production of polyunsaturated fatty acids according to any of claims 1 to 6, wherein a polyunsaturated fatty acid selected from the group

consisting of dihomog- $\gamma$ -linolenic acid, arachidonic acid, eicosapentaenoic acid, docosapentaenoic acid and docosahexaenoic acid is produced in the process.

- 5 8. The process for the production of polyunsaturated fatty acids according to any of claims 1 to 7, wherein the organism is a microorganism, a nonhuman animal or a plant.
9. The process for the production of polyunsaturated fatty acids according to any of claims 1 to 8, wherein the organism is a transgenic plant.
10. The process for the production of polyunsaturated fatty acids according to any of claims 1 to 9, wherein the transgenic plant is an oil crop plant.
- 10 11. An isolated nucleic acid sequence selected from the group consisting of:
- a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18 or SEQ ID NO: 20,
- 15 b) nucleic acid sequences which, as the result of the degeneracy of the genetic code, can be derived from the coding sequence in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18 or SEQ ID NO: 20,
- 20 c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18 or SEQ ID NO: 20, which code for polypeptides with the amino acid sequence shown in SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19 or SEQ ID NO: 21 and which have at least 40% homology at the amino acid level with SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19 or SEQ ID NO: 21 and have lysophosphatidic acid acyltransferase activity.
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- 30 12. An isolated nucleic acid sequence selected from the group consisting of:
- a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 22, SEQ ID NO: 24 or SEQ ID NO: 26,
- b) nucleic acid sequences which, as the result of the degeneracy of the genetic code, can be derived from the coding sequence in SEQ ID NO: 22, SEQ ID NO: 24 or SEQ ID NO: 26,
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- 5 c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 22, SEQ ID NO: 24 or SEQ ID NO: 26, which code for polypeptides with the amino acid sequence shown in SEQ ID NO: 23, SEQ ID NO: 25 or SEQ ID NO: 27 and have at least 40% homology at the amino acid level with SEQ ID NO: 23, SEQ ID NO: 25 or SEQ ID NO: 27 and have glycerol-3-phosphate acyltransferase activity.
13. An isolated nucleic acid sequence selected from the group consisting of:
- 10 a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 28, SEQ ID NO: 30 or SEQ ID NO: 32,
- b) nucleic acid sequences which, as the result of the degeneracy of the genetic code, can be derived from the coding sequence in SEQ ID NO: 28, SEQ ID NO: 30 or SEQ ID NO: 32,
- 15 c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 28, SEQ ID NO: 30 or SEQ ID NO: 32, which code for polypeptides with the amino acid sequence shown in SEQ ID NO: 29, SEQ ID NO: 31 or SEQ ID NO: 33 and have at least 40% homology at the amino acid level with SEQ ID NO: 29, SEQ ID NO: 31 or SEQ ID NO: 33 and which have diacylglycerol acyltransferase activity.
14. An isolated nucleic acid sequence selected from the group consisting of:
- 20 a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 34 or SEQ ID NO: 36,
- b) nucleic acid sequences which, as the result of the degeneracy of the genetic code, can be derived from the coding sequence in SEQ ID NO: 34 or SEQ ID NO: 36,
- 25 c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 34 or SEQ ID NO: 36, which code for polypeptides with the amino acid sequence shown in SEQ ID NO: 35 or SEQ ID NO: 37 and which have at least 40% homology at the amino acid level with SEQ ID NO: 35 or SEQ ID NO: 37 and have lecithin cholesterol acyltransferase activity.
- 30 15. The isolated nucleic acid sequence according to any of claims 11 to 14, which sequence originates from a eukaryote.
16. An amino acid sequence which is encoded by an isolated nucleic acid sequence according to any of claims 11 to 14.
- 35 17. A gene construct comprising an isolated nucleic acid according to any of claims 11 to 14, where the nucleic acid is linked functionally to one or more regulatory signals.

18. The gene construct according to claim 17, wherein the nucleic acid construct comprises additional biosynthesis genes of the fatty acid metabolism or lipid metabolism selected from the group consisting of fatty acid metabolism or lipid metabolism selected from the group consisting of acyl-CoA dehydrogenase(s), acyl-ACP[= acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyltransferase(s), acyl-CoA:lysophospholipid acyltransferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenase(s), lipoxygenase(s), triacylglycerol lipase(s), allene oxide synthase(s), hydroperoxide lyase(s) or fatty acid elongase(s).
19. The gene construct according to claim 17 or 18, wherein the nucleic acid construct comprises additional biosynthesis genes of the fatty acid metabolism or lipid metabolism selected from the group consisting of acyl-CoA:lysophospholipid acyltransferase,  $\Delta$ -4-desaturase,  $\Delta$ -5-desaturase,  $\Delta$ -6-desaturase,  $\Delta$ -8-desaturase,  $\Delta$ -9-desaturase,  $\Delta$ -12-desaturase,  $\Delta$ -5-elongase,  $\Delta$ -6-elongase or  $\Delta$ -9-elongase.
20. A vector comprising a nucleic acid according to any of claims 11 to 14 or a gene construct according to any of claims 17 to 19.
21. A transgenic nonhuman organism comprising at least one nucleic acid according to any of claims 11 to 14, a gene construct according to any of claims 17 to 19 or a vector according to claim 20.
22. The transgenic nonhuman organism according to claim 21, wherein the organism is a microorganism, a nonhuman animal or a plant.
23. The A transgenic nonhuman organism according to claim 21 or 22, wherein the organism is a plant.
24. An oil, a lipid or a fatty acid or a fraction of these, produced by the process according to any of claims 1 to 10.
25. An oil, a lipid or a fatty acid composition comprising polyunsaturated fatty acids prepared by a process according to any of claims 1 to 10 and originating from transgenic plants.
26. The use of oil, lipids or fatty acids produced by a process according to any of claims 1 to 10 or of an oil, lipid or fatty acid composition according to claim 25 in feed, foodstuffs, cosmetics or pharmaceuticals.